

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/579,104  
Source: FWP  
Date Processed by STIC: 5/23/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

10/579,104

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/579,104

DATE: 05/23/2006  
TIME: 14:05:52

Input Set : A:\753-65 PCT-US Sequence Listing.txt  
Output Set: N:\CRF4\05232006\J579104.raw

*Suggestion:  
Consult  
Sequence Rules*

3 <110> APPLICANT: POLYPHOR LTD.  
5 <120> TITLE OF INVENTION: Template fixed beta-hairpin mimetics and their use in  
6 phage display  
8 <130> FILE REFERENCE: P1338PCT  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,104  
C--> 11 <141> CURRENT FILING DATE: 2006-05-12  
13 <160> NUMBER OF SEQ ID NOS: 44  
15 <170> SOFTWARE: PatentIn Ver. 2.1

*pp 1-6*

## ERRORED SEQUENCES

729 <210> SEQ ID NO: 43  
730 <211> LENGTH: 16  
731 <212> TYPE: PRT  
732 <213> ORGANISM: Artificial Sequence  
W--> 733 <220> FEATURE: *in L2207-2223 section*  
733 <223> OTHER INFORMATION: Cysteine residues in positions 3 and 14 are linked  
734 by a disulfide bridge  
E--> 736 <400> SEQUENCE: 42  
W--> 737 Glu Thr Cys Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa Xaa Xaa Thr Lys  
738 1 5 10 15

**Does Not Comply  
Corrected Diskette Needed**

*L2207 insert this mandatory numeric identifier*

*Xaa's need explanation  
in L2207-2223 section*

*Xaa is at  
position 14*

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SEQUENCE LISTING

expose <110> POLYPHOR LTD.  
with <120> Template fixed beta-hairpin mimetics and their use in  
phage display  
↓  
<130> P1338PCT  
1507 <140> PCT/EP 03/12783  
1517 <141> 2003-11-15

These are prior data

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3

<210> 1  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence, key sequence

<400> 1  
Val Arg Lys Lys  
1

Insufficient  
Explanation - give  
source

(see item 11 on  
Error summary  
sheet)

This type of error  
appears in  
subsequent  
sequences, too.

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<210> 42  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DNA sequence of  
randomized template fixed beta-hairpin mimetic  
Phage library

<220>  
<221> CDS  
<222> (1)..(48)

<220>  
<223> Xaa in the peptide chain signifies randomized  
amino acid positions

<220>  
<223> Cysteine residues in positions 3 and 14 are linked  
by a disulfide bridge

<400> 42  
gaa acc tgc nnk nnk nnk cgt ggt gac nnk nnk nnk thc acc aaa 48

h's need explanation in 2227-2237  
section

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<210> 44  
<211> 84  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:olignucleotide  
for library construction

<400> 44  
catgtttcgg ccgagccacc acctttggtg cagggggggg ggggggcacc acgggggggg 60  
gggcagggtt cagagtgaga atag 84

nls need exploration

6

VARIABLE LOCATION SUMMARY  
PATENT APPLICATION: US/10/579,104

DATE: 05/23/2006  
TIME: 14:05:53

Input Set : A:\753-65 PCT-US Sequence Listing.txt  
Output Set: N:\CRF4\05232006\J579104.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:7; Xaa Pos. 4,5

Seq#:42; N Pos. 10,11,13,14,16,17,28,29,31,32,34,35,37,38

Seq#:42; Xaa Pos. 4,5,6,10,11,12,13,14

Seq#:43; Xaa Pos. 4,5,6,10,11,12,13,14

Seq#:44; N Pos. 34,35,37,38,40,41,43,44,55,56,58,59,61,62



**VERIFICATION SUMMARY**  
**PATENT APPLICATION: US/10/579,104**

**DATE: 05/23/2006**  
**TIME: 14:05:53**

**Input Set : A:\753-65 PCT-US Sequence Listing.txt**  
**Output Set: N:\CRF4\05232006\J579104.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:114 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7  
L:114 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7  
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0  
M:341 Repeated in SeqNo=42  
L:733 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43  
L:736 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:43  
L:737 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:43  
L:737 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:43  
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0  
L:752 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:44  
L:752 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:44  
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0  
M:341 Repeated in SeqNo=44